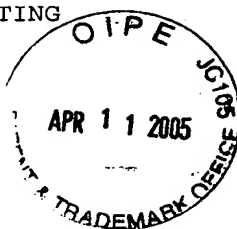


SEQUENCE LISTING



(1) GENERAL INFORMATION:

(i) APPLICANT: Oon, Chong Jin
Lim, Gek Keow
Leong, Ai Lin
Zhao, Yi
Chen, Wei Ning

(ii) TITLE OF INVENTION: A VACCINE-INDUCED HEPATITIS B VIRAL STRAIN AND USES THEREOF

(iii) NUMBER OF SEQUENCES: 11

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Ladas & Parry
(B) STREET: 26 West 61 Street
(C) CITY: New York
(D) STATE: New York
(E) COUNTRY: USA
(F) ZIP: 10023

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 09/719,533
(B) FILING DATE: 13-DEC-2000
(C) CLASSIFICATION: 435

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: PCT/SG98/00045
(B) FILING DATE: 19-JUN-1998

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Mass, Clifford J.
(B) REGISTRATION NUMBER: 30,086
(C) REFERENCE/DOCKET NUMBER: U-013108-9

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (212) 708-1890

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3215 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CTCCACCACT TTCCACCAAA CTCTTCAAGA TCCCAGAGTC AGGGCCCTGT ACTTTCCTGC	60
TGGTGGCTCC AGTTCAGGAA CAGTGAGCCC TGCTCAGAAT ACTGTCTCTG CCATATCGTC	120

AATCTTATCG	AAGACTGGGG	ACCCTGTACC	GAACATGGAG	AACATCGCAT	CAGGACTCCT	180
AGGACCCCTG	CTCGTGTTAC	AGGCGGGGTT	TTTCTTGTTG	ACAAAAATCC	TCACAATACC	240
GCAGAGTCTA	GACTCGTGGT	GGA CT TCTCT	CAATTTTCTA	GGGGGAACAC	CCGTGTGTCT	300
TGGCCAAAAT	TCGCAGTCCC	AAATCTCCAG	TCACTCACCA	ACCTGTTGTC	CTCCAATTTG	360
TCCTGGTTAT	CGCTGGATGT	GTCTGCGGCG	TTTTATCATC	TTCCTCTGCA	TCCTGCTGCT	420
ATGCCTCATC	TTCTTGTTGG	TTCTTCTGGA	CTATCAAGGT	ATGTTGCCCG	TTTGTCTCT	480
AATTCCAGGA	TCAACAACAA	CCAGCACC GG	ACCATGCAAA	ACCTGCACAA	CTCCTGCTCA	540
AGGAACCTCT	ATGTTTCCCT	CATGTTGCTG	TACAAAACCT	ACGGACAGAA	ACTGCACCTG	600
TATTCCCATC	CCATCATCTT	GGGCTTTCGC	AAAATACCTA	TGGGAGTGGG	CCTCAGTCCG	660
TTTCTCTTGG	CTCAGTTTAC	TAGTGCCATT	TGTT CAGTGG	TTCGTAGGGC	TTTCCCCCAC	720
TGTCTGGCTT	TCAGTTATAT	GGATGATGTG	GTTTTGGGGG	CCAAGTCTGT	ACAACATCTT	780
GAGTCCCTTT	ATGCCGCTGT	TACCAATTTT	CTTTTGTCTT	TGGGTATACA	TTTAAACCCT	840
CACAAAACAA	AAAGATGGGG	ATATTCCCTT	AACTTCATGG	GATATGTCAT	TGGGAGTTGG	900
GGCACATTGC	CACAGGAACA	TATTGTACAA	AAAATCAAAA	TGTGTTTTAG	GAAACTTCCT	960
GTAAACAGGC	CTATTGATTG	GAAAGTATGT	CAACGAATTG	TGGGTCTTTT	GGGGTTTGCC	1020
CCCCCTTTCA	CGCAATGTGG	ATATCCTGCT	TTAATGCCTT	TATATGCATG	TATACAAGCA	1080
AAACAGGCTT	TTACTTTCTC	GCAAACCTTAC	AAGACCTTTC	TAAGTAAACA	GTATCTGAAC	1140
CTTTACCCCG	TTGCTCGGCA	ACGCCCTGGT	CTGTGCCAAG	TGTTTGCTGA	CGCAACCCCC	1200
ACTGGTTGGG	GCTTGGCCAT	AGGCCATCAG	CGCATGCGTG	GAACCTTTGT	GTCTCCTCTG	1260
CCGATCCATA	CTGCGGAACT	CCTAGCCGCT	TGTTTTGCTC	GCAGCAGGTC	TGGGGCAAAA	1320
CTCATCGGGA	CTGACAATTC	TGTCGTGCTC	TCCCGCAAGT	ATACATCATT	TCCATGGCTG	1380
CTAGGCTGTG	CTGCCAACTG	GATCCTGCGC	GGGACGTCCT	TTGTTTACGT	CCCGTCGGCG	1440
CTGAATCCCG	CGGACGACCC	CTCCCGGGGC	CGCTTGGGGC	TCTACCGCCC	GCTTCTCCGC	1500
CTGTTATACC	GACCGACCAC	GGGGCGCACC	TCTCTTTACG	CGGACTCCCC	GTCTGTGCCT	1560
TCTCATCTGC	CGGACCGTGT	GCACTTCGCT	TCACCTCTGC	ACGTCGCATG	GAGACCACCG	1620
TGAACGCCCA	CGGGAACCTG	CCCAAGGTCT	TGCATAAGAG	GACTCTTGGA	CTTTCAGCAA	1680
TGTCAACGAC	CGACCTTGAG	GCATACTTCA	AAGACTGTGT	GTTTAATGAG	TGGGAGGAGT	1740
TGGGGGAGGA	GGTTAGGTTA	AAGGTCTTTG	TACTAGGAGG	CTGTAGGCAT	AAATTGGTGT	1800
GTTCAACATC	ACCATGCAAC	TTTTTCACCT	CTGCCTAATC	ATCTCATGTT	CATGTCCTAC	1860
TGTTCAAGCC	TCCAAGCTGT	GCCTTGGGTG	GCTTTGGGGC	ATGGACATTG	ACCCGTATAA	1920

AGAATTTGGA GCTTCTGTGG AGTTACTCTC TTTTTTGCCT TCTGACTTTT TTCCTTCTAT	1980
TCGAGATCTC CTCGACACCG CCTCTGCTCT GTATCGGGAG GCCTTAGAGT CTCCGGAACA	2040
TTGTTACCT CACCATACGG CACTCAGGCA AGCTATTCTG AGTTGGGGTG AGTTAATGAA	2100
TCTAGCCACC TGGGTGGGAA GTAATTTGGA AGATCCAGCA TCCAGGGAAT TAGTAGTCAG	2160
CTATGTCAAC GTTAATATGG GCCTAAAAAT CAGACAATA TTGTGGTTTC ACATTTCTCTG	2220
TCTTACTTTT GGGAGAGAAA CTGTTCTTGA ATATTTGGTG TCTTTTGGAG TGTGGATTCTG	2280
CACTCCTCCT GCATATAGAC CACCAAATGC CCCTATCTTA TCAACACTTC CGGAAACTAC	2340
TGTTGTTAGA CGAAGAGGCA GGTCCCCTAG AAGAAGAACT CCCTCGCCTC GCAGACGAAG	2400
GTCTCAATCG CCGCGTCGCA GAAGATCTCA ATCTCGGGAA TCTCAATGTT AGTATTCCTT	2460
GGACACATAA GGTGGGAAAC TTTACGGGGC TTTATTCTTC TACGGTACCT TGCTTTAATC	2520
CTAAATGGCA AACTCCTTCT TTTCCGGACA TTCATTTGCA GGAGGACATT CTTGATAGAT	2580
GTAAGCAATT TGTGGGGCCC CTTACAGTAA ATGAAAACAG GAGACTAAAA TTAATTATGC	2640
CTGCTAGGTT TTATCCAAAT GTTACTAAAT ATTTGCCCTT AGATAAAGGG ATCAAACCAT	2700
ATTATCCAGA GTATGTAGTT AATCATTACT TCCAGACGCG ACATTATTTA CAACTCTTT	2760
GGAAGGCGGG GATCTTATAT AAAAGAGAGT CCACACGTAG CGCCTCATTT TGCGGGTCAC	2820
CATATTCTTG GGAACAAGAT CTACAGCATG GGAGGTTGGT CTTCCAAACC TCGAAAAGGC	2880
ATGGGGACAA ATCTTTCTGT CCCCAATCCC CTGGGATTCT TCCCCGATCA TCAGTTGGAC	2940
CCTGCATTCA AAGCCAACTC AGAAAATCCA GATTGGGACC TCAACCCGCA CAAGGACAAC	3000
TGGCCGGACG CCAACAAGGT GGGAGTGGGA GCATTGCGGC CAGGGTTCAC CCCTCCTCAT	3060
GGGGGACTGT TGGGGTGGAG CCCTCAGGCT CAGGGCCTAC TCACAACTGT GCCAGCAGCT	3120
CCTCCTCTG CCTCCACCAA TCGGCAGTCA GGAAGGCAGC CTACTCCCTT ATCTCCACCT	3180
CTAAGGGACA CTCATCCTCA GGCCATGCAG TGGAA	3215

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 843 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Pro	Leu	Ser	Tyr	Gln	His	Phe	Arg	Lys	Leu	Leu	Leu	Leu	Asp	Glu
1				5					10					15	

Glu Ala Gly Pro Leu Glu Glu Glu Leu Pro Arg Leu Ala Asp Glu Gly
 20 25 30

Leu Asn Arg Arg Val Ala Glu Asp Leu Asn Leu Gly Asn Leu Asn Val
 35 40 45

Ser Ile Pro Trp Thr His Lys Val Gly Asn Phe Thr Gly Leu Tyr Ser
 50 55 60

Ser Thr Val Pro Cys Phe Asn Pro Lys Trp Gln Thr Pro Ser Phe Pro
 65 70 75 80

Asp Ile His Leu Gln Glu Asp Ile Leu Asp Arg Cys Lys Gln Phe Val
 85 90 95

Glu Pro Leu Thr Val Asn Glu Asn Arg Arg Leu Lys Leu Ile Met Pro
 100 105 110

Ala Arg Phe Tyr Pro Asn Val Thr Lys Tyr Leu Pro Leu Asp Lys Gly
 115 120 125

Ile Lys Pro Tyr Tyr Pro Glu Tyr Val Val Asn His Tyr Phe Gln Thr
 130 135 140

Arg His Tyr Leu His Thr Leu Trp Lys Ala Gly Ile Leu Tyr Lys Arg
 145 150 155 160

Glu Ser Thr Arg Ser Ala Ser Phe Cys Gly Ser Pro Tyr Ser Trp Glu
 165 170 175

Gln Asp Leu Gln His Gly Arg Leu Val Phe Gln Thr Ser Lys Arg His
 180 185 190

Gly Asp Lys Ser Phe Cys Pro Glu Ser Pro Gly Ile Leu Pro Arg Ser
 195 200 205

Ser Val Gly Pro Cys Ile Gln Ser Gln Leu Arg Lys Ser Arg Leu Gly
 210 215 220

Pro Gln Pro Ala Gln Gly Gln Leu Ala Gly Arg Gln Gln Gly Gly Ser
 225 230 235 240

Gly Ser Ile Arg Ala Arg Val His Pro Ser Ser Trp Gly Thr Val Gly
 245 250 255

Val Glu Pro Ser Gly Ser Gly Pro Thr His Asn Cys Ala Ser Ser Ser
 260 265 270

Ser Ser Cys Leu His Gln Ser Ala Val Arg Lys Ala Ala Tyr Ser Leu
 275 280 285

Ile Ser Thr Ser Lys Gly His Ser Ser Ser Gly His Ala Val Glu Leu
 290 295 300

His His Phe Pro Pro Asn Ser Ser Arg Ser Gln Ser Gln Gly Pro Val
 305 310 315 320

Leu Ser Cys Trp Trp Leu Gln Phe Arg Asn Ser Glu Pro Cys Ser Glu
 325 330 335

Tyr Cys Leu Cys His Ile Val Asn Leu Ile Glu Asp Trp Gly Pro Cys
 340 345 350
 Thr Glu His Gly Glu His Arg Ile Arg Thr Pro Arg Thr Pro Ala Arg
 355 360 365
 Val Thr Gly Gly Val Phe Leu Val Asp Lys Asn Pro His Asn Thr Ala
 370 375 380
 Glu Ser Arg Leu Val Val Asp Phe Ser Gln Phe Ser Arg Gly Asn Thr
 385 390 395 400
 Arg Val Ser Trp Pro Lys Phe Ala Val Pro Asn Leu Gln Ser Leu Thr
 405 410 415
 Asn Leu Leu Ser Ser Asn Leu Ser Trp Leu Ser Leu Asp Val Ser Ala
 420 425 430
 Ala Phe Tyr His Leu Pro Leu His Pro Ala Ala Met Pro His Leu Leu
 435 440 445
 Val Gly Ser Ser Gly Leu Ser Arg Tyr Val Ala Arg Leu Ser Ser Asn
 450 455 460
 Ser Arg Ile Asn Asn Asn Glu His Arg Thr Met Glu Asn Leu His Asn
 465 470 475 480
 Ser Cys Ser Arg Asn Leu Tyr Val Ser Leu Met Leu Leu Tyr Lys Thr
 485 490 495
 Tyr Gly Gln Lys Leu His Leu Tyr Ser His Pro Ile Ile Leu Gly Phe
 500 505 510
 Arg Lys Ile Pro Met Gly Val Gly Leu Ser Pro Phe Leu Leu Ala Gln
 515 520 525
 Phe Thr Ser Ala Ile Cys Ser Val Val Arg Arg Ala Phe Pro His Cys
 530 535 540
 Leu Ala Phe Ser Tyr Met Asp Asp Val Val Leu Gly Ala Lys Ser Val
 545 550 555 560
 Gln His Leu Glu Ser Leu Tyr Ala Ala Val Thr Asn Phe Leu Leu Ser
 565 570 575
 Leu Gly Ile His Leu Asn Pro His Lys Thr Lys Arg Trp Gly Tyr Ser
 580 585 590
 Leu Asn Phe Met Gly Tyr Val Ile Gly Ser Trp Gly Thr Leu Pro Gln
 595 600 605
 Glu His Ile Val Gln Lys Ile Lys Met Cys Phe Arg Lys Leu Pro Val
 610 615 620
 Asn Arg Pro Ile Asp Trp Lys Val Cys Gln Arg Ile Val Gly Leu Leu
 625 630 635 640
 Gly Phe Ala Ala Pro Phe Thr Gln Cys Gly Tyr Pro Ala Leu Met Pro
 645 650 655

Leu	Tyr	Ala	Cys	Ile	Gln	Ala	Lys	Gln	Ala	Phe	Thr	Phe	Ser	Gln	Thr		
			660					665					670				
Tyr	Lys	Thr	Phe	Leu	Ser	Lys	Gln	Tyr	Leu	Asn	Leu	Tyr	Pro	Val	Ala		
		675					680					685					
Arg	Gln	Arg	Pro	Gly	Leu	Cys	Glu	Val	Phe	Ala	Asp	Ala	Thr	Pro	Thr		
	690					695					700						
Gly	Trp	Gly	Leu	Ala	Ile	Gly	His	Gln	Arg	Met	Arg	Gly	Thr	Phe	Val		
705					710					715					720		
Ser	Pro	Leu	Pro	Ile	His	Thr	Ala	Glu	Leu	Leu	Ala	Ala	Cys	Phe	Ala		
				725					730					735			
Arg	Ser	Arg	Ser	Gly	Ala	Lys	Leu	Ile	Gly	Thr	Asp	Asn	Ser	Val	Val		
			740					745					750				
Leu	Ser	Arg	Lys	Tyr	Thr	Ser	Phe	Pro	Trp	Leu	Leu	Gly	Cys	Ala	Ala		
		755					760					765					
Asn	Trp	Ile	Leu	Arg	Gly	Thr	Ser	Phe	Val	Tyr	Val	Pro	Ser	Ala	Leu		
	770					775					780						
Asn	Pro	Ala	Asp	Asp	Pro	Ser	Arg	Gly	Arg	Leu	Gly	Leu	Tyr	Arg	Pro		
785					790					795					800		
Leu	Leu	Arg	Leu	Leu	Tyr	Arg	Pro	Thr	Thr	Gly	Arg	Thr	Ser	Leu	Tyr		
			805						810					815			
Ala	Asp	Ser	Pro	Ser	Val	Pro	Ser	His	Leu	Pro	Asp	Arg	Val	His	Phe		
			820					825					830				
Ala	Ser	Pro	Leu	His	Val	Ala	Trp	Arg	Pro	Pro							
		835					840										

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met	Gly	Gly	Trp	Ser	Ser	Lys	Pro	Arg	Lys	Gly	Met	Gly	Thr	Asn	Leu		
1				5					10					15			
Ser	Val	Pro	Asn	Pro	Leu	Gly	Phe	Phe	Pro	Asp	His	Gln	Leu	Asp	Pro		
			20					25					30				
Ala	Phe	Lys	Ala	Asn	Ser	Glu	Asn	Pro	Asp	Trp	Asp	Leu	Asn	Pro	His		
		35					40					45					

Lys	Asp	Asn	Trp	Pro	Asp	Ala	Asn	Lys	Val	Gly	Val	Gly	Ala	Phe	Gly		
50						55					60						
Pro	Gly	Phe	Thr	Pro	Pro	His	Gly	Gly	Leu	Leu	Gly	Trp	Ser	Pro	Gln		
65					70					75					80		
Ala	Gln	Gly	Leu	Leu	Thr	Thr	Val	Pro	Ala	Ala	Pro	Pro	Pro	Ala	Ser		
			85						90					95			
Thr	Asn	Arg	Gln	Ser	Gly	Arg	Gln	Pro	Thr	Pro	Leu	Ser	Pro	Pro	Leu		
			100					105					110				
Arg	Asp	Thr	His	Pro	Gln	Ala	Met	Gln	Trp	Asn	Ser	Thr	Thr	Phe	His		
		115					120					125					
Gln	Thr	Leu	Gln	Asp	Pro	Arg	Val	Arg	Ala	Leu	Tyr	Phe	Pro	Ala	Gly		
	130					135					140						
Gly	Ser	Ser	Ser	Gly	Thr	Val	Ser	Pro	Ala	Gln	Asn	Thr	Val	Ser	Ala		
145					150					155					160		
Ile	Ser	Ser	Ile	Leu	Ser	Lys	Thr	Gly	Asp	Pro	Val	Pro	Asn	Met	Glu		
				165					170					175			
Asn	Ile	Ala	Ser	Gly	Leu	Leu	Gly	Pro	Leu	Leu	Val	Leu	Gln	Ala	Gly		
			180					185					190				
Phe	Phe	Leu	Leu	Thr	Lys	Ile	Leu	Thr	Ile	Pro	Gln	Ser	Leu	Asp	Ser		
		195					200					205					
Trp	Trp	Thr	Ser	Leu	Asn	Phe	Leu	Gly	Gly	Thr	Pro	Val	Cys	Leu	Gly		
	210					215					220						
Gln	Asn	Ser	Gln	Ser	Gln	Ile	Ser	Ser	His	Ser	Pro	Thr	Cys	Cys	Pro		
225					230					235					240		
Pro	Ile	Cys	Pro	Gly	Tyr	Arg	Trp	Met	Cys	Leu	Arg	Arg	Phe	Ile	Ile		
				245					250					255			
Phe	Leu	Cys	Ile	Leu	Leu	Leu	Cys	Leu	Ile	Phe	Leu	Leu	Val	Leu	Leu		
			260					265					270				
Asp	Tyr	Gln	Gly	Met	Leu	Pro	Val	Cys	Pro	Leu	Ile	Pro	Gly	Ser	Thr		
		275					280					285					
Thr	Thr	Ser	Thr	Gly	Pro	Cys	Lys	Thr	Cys	Thr	Thr	Pro	Ala	Gln	Gly		
	290					295					300						
Thr	Ser	Met	Phe	Pro	Ser	Cys	Cys	Cys	Thr	Lys	Pro	Thr	Asp	Arg	Asn		
305					310					315					320		
Cys	Thr	Cys	Ile	Pro	Ile	Pro	Ser	Ser	Trp	Ala	Phe	Ala	Lys	Tyr	Leu		
				325					330					335			
Trp	Glu	Trp	Ala	Ser	Val	Arg	Phe	Ser	Trp	Leu	Ser	Leu	Leu	Val	Pro		
			340					345					350				
Phe	Val	Gln	Trp	Phe	Val	Gly	Leu	Ser	Pro	Thr	Val	Trp	Leu	Ser	Val		
		355					360					365					

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met	Ala	Ala	Arg	Leu	Cys	Cys	Gln	Leu	Asp	Pro	Ala	Arg	Asp	Val	Leu	
1				5				10						15		
Cys	Leu	Arg	Pro	Val	Gly	Ala	Glu	Ser	Arg	Gly	Arg	Pro	Leu	Pro	Gly	
			20					25					30			
Pro	Leu	Gly	Ala	Leu	Pro	Pro	Ala	Ser	Pro	Pro	Val	Ile	Pro	Thr	Asp	
		35					40					45				
His	Gly	Ala	His	Leu	Ser	Leu	Arg	Gly	Leu	Pro	Val	Cys	Ala	Phe	Ser	
	50					55					60					
Ser	Ala	Gly	Pro	Cys	Ala	Leu	Arg	Phe	Thr	Ser	Ala	Arg	Arg	Met	Glu	
65					70					75					80	
Thr	Thr	Val	Asn	Ala	His	Gly	Asn	Leu	Pro	Lys	Val	Leu	His	Lys	Arg	
			85						90					95		
Thr	Leu	Gly	Leu	Ser	Ala	Met	Ser	Thr	Thr	Asp	Leu	Glu	Ala	Tyr	Phe	
			100					105					110			
Lys	Asp	Cys	Val	Phe	Asn	Glu	Trp	Glu	Glu	Leu	Gly	Glu	Glu	Val	Arg	
		115					120					125				
Leu	Lys	Val	Phe	Val	Leu	Gly	Gly	Cys	Arg	His	Lys	Leu	Val	Cys	Ser	
	130					135					140					
Pro	Ser	Pro	Cys	Asn	Phe	Phe	Thr	Ser	Ala							
145					150											

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ATAAGCTTATG CCCCTATCTT ATCAACACTT CCGGA

35

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GAGTCTAGAC TCTGCGGTAT TGTGA

25

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GAGTCTAGAC TCGTGGTGGA CTTCT

25

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TGAGAATTCT CACGGTGGTC TCCATGCGAC GT

32

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TTTGTTTACG TCCCGT

16

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CTAAGCTTAG TTTCCGGAAG TGTTGAT